Freeform Search

09/818,086

Database:
- US Pre-Grant Publication Full-Text Database
- US Patents Full-Text Database
- US OCR Full-Text Database
- EPO Abstracts Database
- JPO Abstracts Database
- Derwent World Patents Index
- IBM Technical Disclosure Bulletins

Term: L9 and monitor$3

Display: 10 **Documents in Display Format:** - **Starting with Number** 11

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search | Clear | Interrupt

Search History

DATE: Wednesday, June 02, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L11	L10 and marcia	0	L11
L10	L9 and monitor$3	18	L10
L9	L8 and nucleic acid	44	L9
L8	slater.in.	2187	L8
L7	L6 and nucleic acid	1	L7
L6	brankamp.in.	14	L6
L5	L4 and nucleic acid	1	L5
L4	baskin.in.	346	L4
L3	L2 and monitor$3	2	L3
L2	L1 and irradiat$3	2	L2
L1	amplif$7 near5 primer$1 near5 fluorescent near5 sequencing	4	L1

END OF SEARCH HISTORY

Freeform Search

Database:
- US Pre-Grant Publication Full-Text Database
- US Patents Full-Text Database
- US OCR Full-Text Database
- EPO Abstracts Database
- JPO Abstracts Database
- Derwent World Patents Index
- IBM Technical Disclosure Bulletins

Term: monitor$3 near5 amplif$7 near5 sequencing

Display: 10 **Documents in Display Format:** - **Starting with Number** 11

Generate: ○ Hit List ◉ Hit Count ○ Side by Side ○ Image

Search | Clear | Interrupt

Search History

DATE: Wednesday, June 02, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L16	monitor$3 near5 amplif$7 near5 sequencing	2	L16
L15	L14 AND HLA	3	L15
L14	L13 and (HIV or E.coli or Salmonella or Haemophilus)	41	L14
L13	L12 and sequencing	91	L13
L12	monitor$3 near5 amplif$7 near5 fluorescen$2	148	L12
L11	L10 and marcia	0	L11
L10	L9 and monitor$3	18	L10
L9	L8 and nucleic acid	44	L9
L8	slater.in.	2187	L8
L7	L6 and nucleic acid	1	L7
L6	brankamp.in.	14	L6
L5	L4 and nucleic acid	1	L5
L4	baskin.in.	346	L4
L3	L2 and monitor$3	2	L3
L2	L1 and irradiat$3	2	L2
L1	amplif$7 near5 primer$1 near5 fluorescent near5 sequencing	4	L1

09/818086

```
=> s monitor###(10a)amplif######(10a)sequencing
L1            1 MONITOR###(10A) AMPLIF######(10A) SEQUENCING

=> d l1

L1   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2001:196458  CAPLUS
DN   135:367357
TI   Terminal restriction fragment length polymorphism monitoring of genes
     amplified directly from bacterial communities in soils and sediments
AU   Bruce, Kenneth D.; Hughes, Mark R.
CS   Division of Life Sciences, King's College, London, SE1 8WA, UK
SO   Molecular Biotechnology (2000), 16(3), 261-269
     CODEN: MLBOEO; ISSN: 1073-6085
PB   Humana Press Inc.
DT   Journal
LA   English
RE.CNT  45    THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> d l1 bib ab kwic

L1   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2001:196458  CAPLUS
DN   135:367357
TI   Terminal restriction fragment length polymorphism monitoring of genes
     amplified directly from bacterial communities in soils and sediments
AU   Bruce, Kenneth D.; Hughes, Mark R.
CS   Division of Life Sciences, King's College, London, SE1 8WA, UK
SO   Molecular Biotechnology (2000), 16(3), 261-269
     CODEN: MLBOEO; ISSN: 1073-6085
PB   Humana Press Inc.
DT   Journal
LA   English
AB   Terminal Restriction Fragment Length Polymorphism (T-RFLP) or Fluorescent
     Polymerase Chain Reaction/Restriction Fragment Length Polymorphism
     (FluRFLP) have made a significant impact on the way in which PCR products
     amplified from mixed community DNA exts. have been assessed.  Tech., these
     approaches are essentially the same.  PCR products are generated that
     contain at one 5' end label, typically a fluorescent moiety, that will be
     detected by a DNA sequencing machine.  Upon digestion using a specific
     restriction endonuclease, labeled and unlabeled fragments are generated.
     This restriction endonuclease is chosen such that following this
     digestion, each labeled fragment corresponds to a different sequence
     variant.  During electrophoretic separation, the DNA sequencing machine detects
     only these labeled fragments and therefore detects only the sequence
     variants.  The aim of this article is to describe the protocols and
     demonstrate that this profiling can be performed using different DNA
     sequencing machines.  The anal. and applications of this approach are also
     discussed.
RE.CNT  45    THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT
IT   DNA sequence analysis
     Fluorescence
        (PCR products contain at one 5' end a fluorescent moiety, to be
        detected by DNA sequencing machine; terminal restriction
        fragment length polymorphism monitoring of genes
        amplified directly from bacterial communities in soils and
        sediments)


=> s amplif#######(10a)monitor###(10a)fluorescen##
L2          143 AMPLIF#######(10A) MONITOR###(10A) FLUORESCEN##
```

=> s l2 and sequencing
L3 7 L2 AND SEQUENCING

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 5 DUP REM L3 (2 DUPLICATES REMOVED)

=> d l4 1-5 bib ab kwic

L4 ANSWER 1 OF 5 MEDLINE on STN DUPLICATE 1
AN 2002346153 MEDLINE
DN PubMed ID: 12089280
TI Detection of duck hepatitis B virus DNA on filter paper by PCR and SYBR green dye-based quantitative PCR.
AU Wang Chi-Young J; Giambrone Joseph J; Smith Bruce F
CS Department of Poultry Science, College of Veterinary Medicine, Auburn University, Auburn, Alabama 36849, USA.
SO Journal of clinical microbiology, (2002 Jul) 40 (7) 2584-90.
Journal code: 7505564. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200208
ED Entered STN: 20020629
Last Updated on STN: 20020827
Entered Medline: 20020826
AB Duck hepatitis B virus (DHBV) belongs to the Hepadnaviridae family, which includes human Hepatitis B virus (HBV) and Woodchuck hepatitis virus. It is widely distributed in wild and domestic ducks due to congenital transmission. HBV is a worldwide health problem, with carriers at risk of developing cirrhosis and liver cancer. Medical staff and scientists working with HBV must be vaccinated because of its contagious nature. DHBV is a safe surrogate for HBV because of their similarities. Collection of serum and blood samples on filter paper has been used to screen for metabolic disorders, genetic diseases, and viral infection and for evolutionary studies of the genome. In this study, DHBV from serum and blood dried on filters was detected by PCR. A 0.1-microl sample was sufficient for detection. The immobilization potential of filter papers for DHBV was examined, and the highest yield of PCR products was observed with Whatman paper. Dried serum was stable under different storage temperatures for 4 weeks, but the yields of PCR products decreased when the temperature was >or=4 degrees C. The optimal condition for storage was -70 degrees C. A newly developed quantitative PCR based on **monitoring** the **amplification** by measuring the increase in **fluorescence** caused by the binding of SYBR green dye to double-stranded products was applied herein. DHBV genomic DNA cloned in a plasmid was used for the generation of standard DHBV DNA for quantitative PCR. It validated results from PCR in terms of the copy number of DHBV particles. The specificity of PCR was demonstrated by melting curve analysis, and the differentiation of two DHBV isolates amplified from dried serum was demonstrated based on their melting temperatures determined by GC contents and sequence. It was easier and simpler than other PCR-based DNA techniques. The use of serum dried on filters allows samples from distant field for which cold storage and transportation are a problem to be mailed to the diagnostic laboratory. Samples can be archived for comparison and used as a source of DNA for cloning and **sequencing**.
AB . . . was >or=4 degrees C. The optimal condition for storage was -70 degrees C. A newly developed quantitative PCR based on **monitoring** the **amplification** by measuring the increase in **fluorescence** caused by the binding of SYBR green dye to double-stranded products was applied herein. DHBV genomic DNA cloned in

a. . . to the diagnostic laboratory. Samples can be archived for comparison and used as a source of DNA for cloning and **sequencing**
.

L4 ANSWER 2 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:317029 BIOSIS
DN PREV200100317029
TI **Monitoring** of mixed chimerism by a technique using **fluorescence** based PCR **amplification** of microsatellite after allogeneic hematopoietic stem cell transplantation.
AU Saito, Akiko [Reprint author]; Ogawa, Seishi [Reprint author]; Hadama, Tohru; Kinoshita, Moritoshi; Chiba, Shigeru [Reprint author]; Hirai, Hisamaru [Reprint author]
CS Hematology and Oncology, University of Tokyo, Bunkyo-ku, Tokyo, Japan
SO Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 395a. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology. San Francisco, California, USA. December 01-05, 2000. American Society of Hematology.
CODEN: BLOOAW. ISSN: 0006-4971.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 4 Jul 2001
Last Updated on STN: 19 Feb 2002
AB (Introduction) Monitoring of mixed chimerism following hematopoietic stem cell transplantation (HSCT) provides an important clue to evaluate engraftment and to detect graft failure or early relapse. Several techniques have been applied for this purpose; Mixed chimerism after sex-mismatched transplant can be quickly and quantitively assessed by fluorescent in situ hybridization (FISH) analysis using X- and Y-specific probes. Assessment of chimerism in sex-matched transplant has also been possible by differentially detecting a polymorphic allele(s) between the donor and recipient. However, the conventional methods for quantitive detection of polymorphisms such as VNTRs have been frequently too time-consuming in the contexet of clinical applications. In this study we intended to develop a simple method for quickly estimating post-transplant chimerism. (Materials and methods) Genomic DNA was extracted from bone marrow and/or blood samples of 27 donor-recipient pairs following allogeneic HSCT and subjected to the microsatellite PCR analysis, in which three microsatellite loci, D18S51, D20S471 and D22S684, were PCR-amplified using fluorescent primers from the genomic DNAs and length of the PCR products were analyzed using an ABI PRISM 377 automated sequence analyzer. Because the polymorphism in a given locus is represented by the difference in the length of the corresponding PCR products, we first determined the informative loci which showed different electrophoretic mobilities between the donor-recipient pair, and then assessed the chimerism in a given sample by measuring relative intensity of each polymorphic peak for the informative loci. Reliability of this assay was tested by measuring chimerism of the standard DNA samples whose donor/recipient-composition was already known, and by comparing the results with those obtained from other assays, for example, XY-FISH. (Results) In our method, 11 of 11 (100%) cases transplanted from unrelated donors and 13 of 16 (81%) cases from related donors had at least one informative microsatellite locus. Measurement of the standard DNA samples show a linear correlation between the measured values for donor-recipient ratios and the standardized values for the DNA composition. More than 10% of chimera can be stably detected, using as little as ten nanograms of sample DNA. In 11 patients, results from the microsatellite PCR showed excellent concordance with the data obtained from the conventional FISH analysis using X- and Y-specific probes and/or probes detecting tumor-specific translocations. (Conclusions) Fluorescent primer-based microsatellite PCR assay is a feasible, rapid and reliable technique for assessment of mixed chimerism after allogenic HSCT, even with minuscule samples.

TI **Monitoring** of mixed chimerism by a technique using **fluorescence** based PCR **amplification** of microsatellite after allogeneic hematopoietic stem cell transplantation.

IT . . .
hybridization [FISH]: diagnostic method; microsatellite PCR [microsatellite polymerase chain reaction]: DNA amplification, amplification method, fluorescence-based, in-situ recombinant gene expression detection, **sequencing** techniques

IT Miscellaneous Descriptors
chromosomal translocations: tumor-specific; electrophoretic mobility; engraftment; mixed chimerism; Meeting Abstract; Meeting Poster

L4 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:135568 BIOSIS
DN PREV199900135568
TI Identification of Leptospira biflexa by real-time homogeneous detection of rapid cycle PCR product.
AU Woo, T. H. S; Patel, B. K. C. [Reprint author]; Cinco, M.; Smythe, L. D.; Norris, M. A.; Symonds, M. L.; Dohnt, M. F.; Piispanen, J.
CS Sch. Biomol. Biomed. Sci., Fac. Sci., Griffith Univ., Nathan Campus, Brisbane, QLD 4111, Australia
SO Journal of Microbiological Methods, (Feb., 1999) Vol. 35, No. 1, pp. 23-30. print.
CODEN: JMIMDQ. ISSN: 0167-7012.
DT Article
LA English
ED Entered STN: 31 Mar 1999
Last Updated on STN: 31 Mar 1999
AB Sequence analysis of 16S rRNA genes extracted from nucleic acids databases enabled the identification of a Leptospira biflexa (L. biflexa) signature sequence, against which a reverse primer designated L613, was designed. This primer, when used in conjunction with a universal bacterial specific forward primer designated Fd1, enabled the development of a LightCyclerTM-based PCR protocol in which **fluorescence** emission due to binding of SYBR Green I dye to **amplified** products could be detected and **monitored**. A melting temperature (Tm), determined from the melting curve of the amplified product immediately following the termination of thermal cycling, confirmed that the product was that of L. biflexa. Agarose gel electrophoresis therefore was not necessary for identification of PCR products. The PCR protocol was very rapid, and consisted of 30 cycles with a duration of 20 s for each cycle with the monitoring of the melting curve requiring an additional 3 min. The whole protocol was completed in less than 20 min. The PCR protocol was also specific and enabled the identification of 18 strains of L. biflexa, whilst excluding 14 strains of L. interrogans and Leptonema illini. Two examples of its utility in improving work flow of a Leptospira reference laboratory are presented in this article. The use of a simple boiling method for extraction of DNA from all the members of the Leptospiraceae family DNA further simplifies the procedure and makes its use conducive to diagnostic laboratories.
AB. . . conjunction with a universal bacterial specific forward primer designated Fd1, enabled the development of a LightCyclerTM-based PCR protocol in which **fluorescence** emission due to binding of SYBR Green I dye to **amplified** products could be detected and **monitored**. A melting temperature (Tm), determined from the melting curve of the amplified product immediately following the termination of thermal cycling,. . .
IT . . .
analytical method, gel electrophoresis; DNA extraction: Isolation/Purification Techniques: CB, extraction method; LightCycler PCR [polymerase chain reaction]: DNA amplification, amplification method, **sequencing** techniques, in-situ recombinant gene expression detection
IT Miscellaneous Descriptors

nucleotide sequence

L4 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:219054 BIOSIS
DN PREV199900219054
TI Continuous fluorescent monitoring of rapid cycle polymerase chain reaction.
AU Pritham, Gregory H.; Wittwer, Carl T. [Reprint author]
CS Department of Pathology, University of Utah Medical School, 50 N. Medical Drive, Salt Lake City, UT, 84132, USA
SO Journal of Clinical Ligand Assay, (Winter, 1998) Vol. 21, No. 4, pp. 404-412. print.
ISSN: 1081-1672.
DT Article
LA English
ED Entered STN: 7 Jun 1999
Last Updated on STN: 7 Jun 1999
AB Polymerase chain reaction (PCR) amplification and analysis can be performed rapidly. Indeed, both amplification and analysis can occur simultaneously in the same instrument in only 10-30 minutes. Rapid cycle PCR is possible because denaturation, annealing, and extension are fast reactions. Currently, cycling speeds are limited by instrumentation, not chemistry. If rapid cycle PCR is continuously monitored with a fluorimeter, amplification progress can be followed with double-stranded DNA specific dyes or resonance energy transfer probes of multiple designs. Initial template copy number can be determined by monitoring fluorescence once each cycle. Continuous monitoring of fluorescence within a cycle as the temperature is changing can be used to follow product or probe hybridization. Fluorescence melting curves immediately after amplification provide dynamic dot blots of hybridization for product identification or single base genotyping.
IT Methods & Equipment
fluorimeter: laboratory equipment; genotyping: analytical method; polymerase chain reaction: DNA amplification, analytical method, **sequencing** techniques, molecular genetic method, in-situ recombinant gene expression detection; rapid cycle polymerase chain reaction-continuous **fluorescent monitoring**: DNA **amplification**, **sequencing** techniques, molecular genetic method, analytical method, in-situ recombinant gene expression detection
IT Miscellaneous Descriptors
instrumentation; melting curves; mutations: detection; template. . .

L4 ANSWER 5 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1998:472877 BIOSIS
DN PREV199800472877
TI Fluorescence cross-correlation: A new concept for polymerase chain reaction.
AU Rigler, Rudolf [Reprint author]; Foeldes-Papp, Zeno; Meyer-Almes, Franz-Josef; Sammet, Cyra; Voelcker, Martin; Schnetz, Andreas
CS Dep. Med. Biophys., MBB, Karolinska Inst., S-17177 Stockholm, Sweden
SO Journal of Biotechnology, (Aug. 12, 1998) Vol. 63, No. 2, pp. 97-109. print.
CODEN: JBITD4. ISSN: 0168-1656.
DT Article
LA English
ED Entered STN: 5 Nov 1998
Last Updated on STN: 5 Nov 1998
AB In this article we present a new concept for the detection of any specifically amplified target DNA sequences in multiple polymerase chain reactions (PCR) based on fluorescence correlation spectroscopy (FCS). The accumulation of double-stranded target DNA is **monitored** by the cross-correlated **fluorescence** signals provided by two **amplification** primers which are 5'-tagged with two different kinds

of fluorophores (Rhodamine-Green and Cy5). Only the amplified target DNA sequence carrying both primers is observed. Its signal emerges from the background of non-incorporated or non-specifically incorporated primers. Down to 10-25 initial copy numbers of the template in the PCR compartment DNA can presently be detected. No external or internal standards are required for determining the size and the amplified copy number of specific DNA. The PCR amplification process is started with all ingredients in a single compartment (e.g. of a microtiter plate), in which amplification and measurement are performed. This eliminates the need for post-PCR purification steps. The homogeneous one-tube approach does not depend on fluorescence energy transfer between the fluorogenic dyes. Thus, it does not interfere with the enzymatic amplification reaction of PCR and allows the continued use of different conditions for amplifying DNA. The results exemplified by PCR-amplified 217-bp and 389-bp target DNA sequences demonstrate that the analysis based on two-color fluorescence cross-correlation is a powerful method for simplifying the identification of targets in PCR for medical use. For this purpose, an instrument optimized for two-color excitation and detection of two-color emission has been developed, incorporating the principle of confocal arrangement.

AB. . . sequences in multiple polymerase chain reactions (PCR) based on fluorescence correlation spectroscopy (FCS). The accumulation of double-stranded target DNA is **monitored** by the cross-correlated **fluorescence** signals provided by two **amplification** primers which are 5'-tagged with two different kinds of fluorophores (Rhodamine-Green and Cy5). Only the amplified target DNA sequence carrying. . .

IT Methods & Equipment
polymerase chain reaction: DNA amplification, in-situ recombinant gene expression detection, **sequencing** techniques, molecular genetic method; two-color fluorescence cross-correlation spectroscopy: analytical method

IT Miscellaneous Descriptors
biotechnology

=>